Amendments to the Claims

What is claimed is:

1.-84. (**Canceled**)

85. (**New**) A method for managing a biological database, comprising:
    a. receiving a set of biological sequences;
    b. querying a plurality of databases with the set of biological sequences;
    c. receiving query results from the plurality of databases, wherein the query results comprise at least immunohistological data, *in situ* hybridization data, functional data, expression data, and structural data;
    d. storing the query results in a biological database, wherein each sequence in the set of biological sequences is associated with a respective record comprising query results from each of the plurality of databases;
    e. periodically performing steps b-d;
    f. receiving, from a user, a request to view a record of one of the set of biological sequences; and
    g. displaying an executive summary of the record of one of the set of biological sequences.

86. (**New**) The method of claim 85, wherein the set of biological sequences comprises one or more of, nucleic acid sequences and amino acid sequences.

87. (**New**) The method of claim 85, wherein receiving the set of biological sequences comprises receiving the set of biological sequences from a user.

88. (**New**) The method of claim 85, wherein the query results further comprise complementary deoxyribonucleic acid (cDNA) data, expressed sequence tags, and pharmacology data.

89. (New) The method of claim 85, wherein the plurality of databases comprises two or more of National Center for Biotechnology Information (NCBI) databases or other externally curated and maintained specialized databases.

90. (New) The method of claim 85, wherein periodically performing steps b-d comprises performing steps b-d daily.

91. (New) The method of claim 85, further comprising performing one or more bioinformatics functions on the set of biological sequences or the query results.

92. (New) The method of claim 91, wherein the one or more bioinformatics functions comprises one or more of sequence alignment, gene identification, protein identification structure prediction, motif comparison, and biological text analysis.

93. (New) The method of claim 85, wherein displaying an executive summary of the record of one of the set of biological sequences comprises formatting the requested record for output to the user.

94. (New) A method for managing a biological database, comprising:
   a. providing a plurality of databases;
   b. determining the version of each of the plurality of databases;
   c. determining if the version of each of the plurality of databases is a current version;
   d. downloading the current version of any of the plurality of databases that is not a current version;
   e. periodically performing b-d;
   f. receiving a set of biological sequences;
   g. querying the plurality of databases with the set of biological sequences;

    h. receiving query results from the plurality of databases, wherein the query results comprise at least immunohistological data, *in situ* hybridization data, functional data, expression data, and structural data;

    i. storing the query results in a biological database, wherein each sequence in the set of biological sequences is associated with a respective record comprising query results from each of the plurality of databases;

    j. periodically performing steps b-d;

    k. receiving, from a user, a request to view a record of one of the set of biological sequences; and

    l. displaying an executive summary of the record of one of the set of biological sequences.

95. (New) The method of claim 94, wherein the plurality of databases comprises two or more of, National Center for Biotechnology Information (NCBI) databases or other externally curated and maintained specialized databases.

96. (New) The method of claim 94, wherein periodically performing steps b-d comprises performing steps b-d daily.

97. (New) The method of claim 94, wherein the set of biological sequences comprises one or more of, nucleic acid sequences and amino acid sequences.

98. (New) The method of claim 94, wherein receiving the set of biological sequences comprises receiving the set of biological sequences from a user.

99. (New) The method of claim 94, wherein the query results further comprise complementary deoxyribonucleic acid (cDNA) data, expressed sequence tags, and pharmacology data.

100.   (New) The method of claim 94, further comprising performing one or more bioinformatics functions on the set of biological sequences or the query results.

101.   (New) The method of claim 100, wherein the one or more bioinformatics functions comprises one or more of sequence alignment, gene identification, protein identification structure prediction, motif comparison, and biological text analysis.

102.   (New) The method of claim 94, wherein displaying an executive summary of the record of one of the set of biological sequences comprises formatting the requested record for output to the user.

103.   (New) A system for managing a biological database, comprising:

a target database node, configured to receive and store query results in the biological database, wherein the biological database comprises a set of biological sequences and wherein the query results comprise at least immunohistological data, *in situ* hybridization data, functional data, expression data, and structural data;

a query node, configured to periodically download and store a plurality of databases from an external network;

a functional node, configured to periodically query the plurality of databases on the query database node with the set of biological sequences from the target database node and send query results to the target database node; and

a network switch node configured to direct the receipt and storage of query results in the biological database, the periodic download and storage of the plurality of databases, and the periodic query of the plurality of databases on the query database node.

104.   (New) The system of claim 103, wherein the set of biological sequences comprises one or more of, nucleic acid sequences and amino acid sequences.

105.   (New) The system of claim 103, wherein the functional node is further configured to perform one or more bioinformatics functions on the set of biological sequences or the query results and update the target database node.

106.   (New) The system of claim 104, wherein the one or more bioinformatics functions comprises one or more of sequence alignment, gene identification, protein identification structure prediction, motif comparison, and biological text analysis.

107.   (New) The system of claim 103, wherein the plurality of databases comprises two or more of, National Center for Biotechnology Information (NCBI) databases or other externally curated and maintained specialized databases.

108.   (New) The system of claim 103, wherein the query node is further configured to periodically download and store a plurality of databases from an external network daily.

109.   (New) The system of claim 103, wherein the query results further comprise complementary deoxyribonucleic acid (cDNA) data, expressed sequence tags, and pharmacology data.

110.   (New) The system of claim 103, wherein each of sequences in the set of biological sequences is associated with a record comprising query results from each of the plurality of databases

111.   (New) The system of claim 110, wherein the target database node is further configured to:
          receive, from a user, a request to view a record of one of the set of biological
                    sequences; and

display an executive summary of the record of one of the set of biological sequences.

112.   (New) The system of claim 111, wherein the target database node is further configured to format the requested record for output to the user.